

EVOLUTION OF RACES OF *Colletotrichum lindemuthianum* THAT OCCUR IN SOME REGIONS OF BRAZIL

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Out of 118 isolates collected in different regions of Brazil, Rava et al. (1994) identified and classified 25 races of *Colletotrichum lindemuthianum* by inoculation on 12 differential cultivars (Pastor-Corrales, 1992). Alzate-Marin et al. (1997) used RAPD (Random Amplified Polymorphic DNA) to evaluate the genetic diversity of 22 of these races. Three distinct groups were identified: group I (races 585, 72, 23, 73, and 79), group II (races 339, 343, 67, 64, 87, 95, 81, 65, 89, 97, 453, 117, 119, 55, 7, and 83) and group III (race 102). A evolution model was designed by combining the virulence and the molecular data (Figure 1). The model was constructed based on two premises: presence of common RAPD bands indicate genetic similarity among the races, and a new race appears as a result of gain of a specific virulence gene.

In this model, the virulence genes are designated by letters (a to l) according to the compatibility reactions of the races with each one of the 12 common bean differential cultivars. For instance, virulence genes *a* and *b* are compatible with resistance genes of Michelite and DRK, respectively. Virulence gene *j* is compatible with resistance gene *Mex. III* of cultivar TU and so on (Tamayo et al., 1995). Virulence genes *k* and *l* were not included in this model because cultivars AB 136 and G 2333 are resistant to all 25 races identified in Brazil.

All races used in this study were obtained from small-seeded bean varieties of Middle American origin, suggesting that these races co-evolved with Middle American bean cultivars. The virulence data show that *C. lindemuthianum* in Brazil is highly diversified as it attacks a broad range of Andean and Middle American differential cultivars. Similar observations were reported by Pastor-Corrales (BIC-1996) for races that occur in Mexico and Central America where the pathogen races and the cultivars are also Middle American.

According to the model, races 8 and 64 that infect cultivars Cornell 49-242 (gene *Are*) and Mexico 222 (gene *Mex. I*), respectively, are the origins of two important evolution routes of this pathogen.

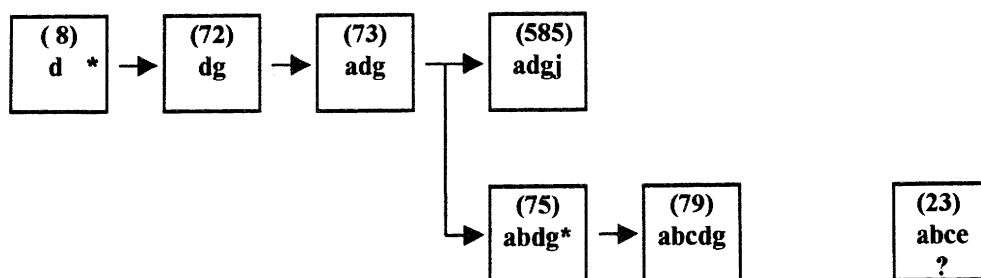
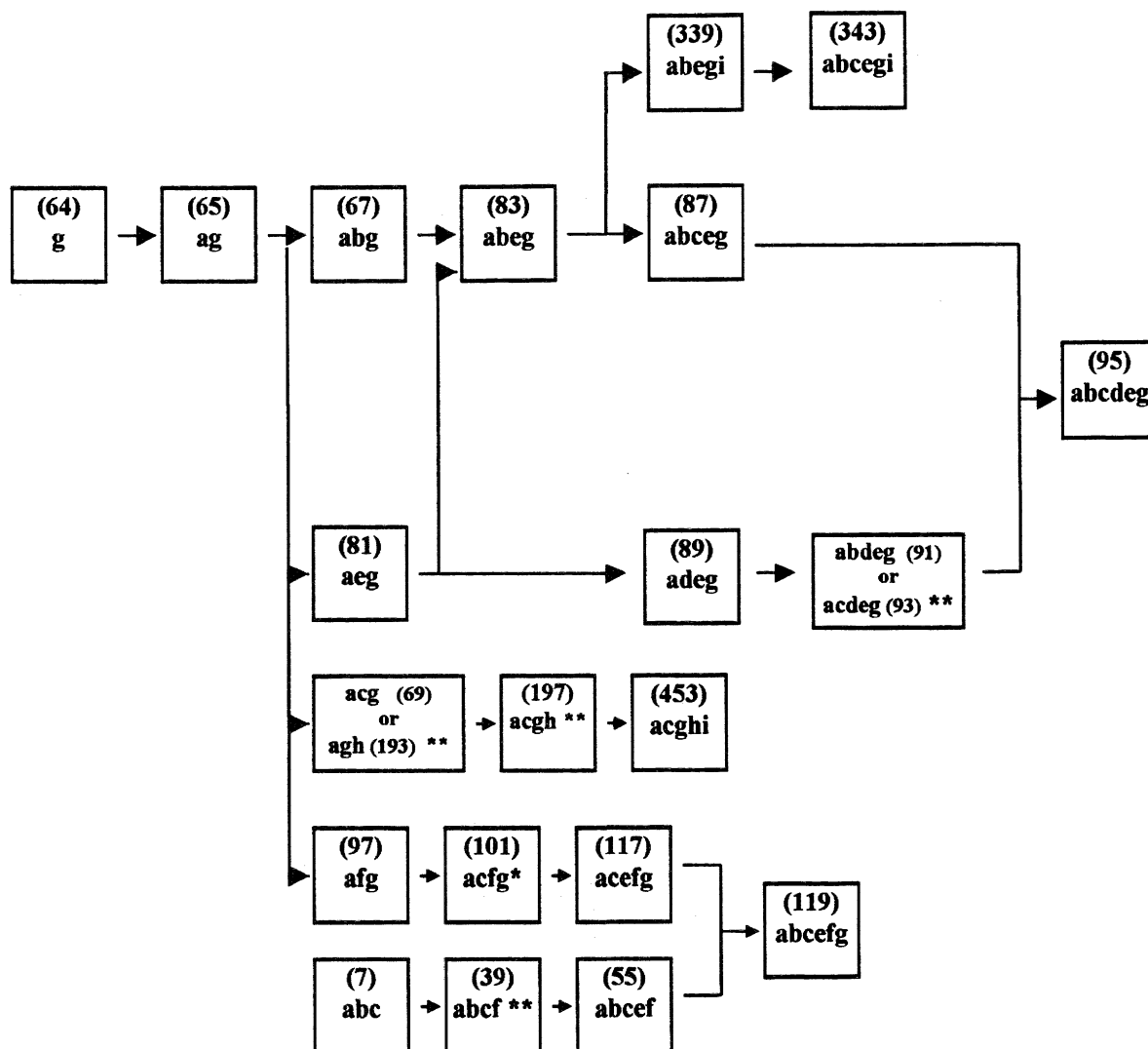
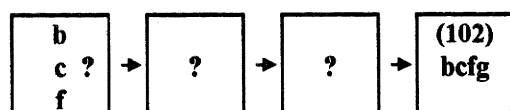
The race groups 95-119-343, 79-453 and 102-585 present a great risk to common bean crop in Brazil, since they have 6, 5 and 4 virulence genes, respectively. These races can attack a great number of cultivars that have some of the following resistance genes: *A* (*Co-1*), *Are* (*Co-2*), *Mex. I* (*Co-3*), *Mex. II* (*Co-4*) or *Mex. III* (*Co-5*) (LIST of Genes, BIC-1996). In this way, all these races have compatible reactions with *Mex. I* and *A* resistance genes (except 453 and 585). Races 79, 95 and 585 have compatible reactions with resistance gene *Are*, races 453 and 343 have compatible reactions with resistance gene *Mex. II* and 585 with *Mex. III* resistance gene. Therefore, the incorporation and pyramiding of new resistant genes, for example *Co-6* or *Co-7* of AB 136 and G 2333 cultivars, respectively, will be an important strategy for stabilizing resistance against anthracnose of common bean.

The model leads to the conclusion that races 39, 69, 91, 93, 193 and 197 are possibly present in Brazil although they were not identified by Rava et al. (1994). In that sense, our group recently identified race 69 in the state of Minas Gerais (Mesquita et al., 1997).

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REFERENCES

- Alzate-Marin, A. L. et al. (1997). Fitopatol. bras. 22(1):85-88.
- List of genes (1996). BIC. 39:3.
- Mesquita, A. G. G. et al. (1997). Fitopatol. bras. 22 (supplement):285.
- Pastor-Corrales, M. A. (1992). Doc. de Trabajo n° 113. CIAT, Cali, Colombia. p. 212-239.
- Pastor-Corrales, M. A. (1996). BIC. 39:46.
- Rava, C. et al. (1994). Fitopatol. bras. 19:167-172.
- Tamayo, P. J. et al. (1995). Fitopatologia Colombiana 19:1-6.

RAPD GROUP I**RAPD GROUP II****RAPD GROUP III**

* DNA from *C. lindemuthianum* races 8, 75 and 101 was not amplified.

**Races proposed. The numbers refer to the binary classification of the pathogen and the letters to their respective virulence phenotype.

Figure 1. Proposed model for the evolution of the 25 races of *C. lindemuthianum* identified in Brazil based on pathogenicity phenotypes and RAPD analyses.